BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

As rescanning documents *will not* correct images, please do not report the images to the Image Problem Mailbox.

ATTENUATED MICROORGANISMS FOR THE TREATMENT OF INFECTION

Field of the Invention

This invention relates to attenuated microorganisms that can be used in vaccine compositions for the prevention or treatment of bacterial or viral infections.

Background to the Invention

It is well established that live attenuated micro-organisms are highly effective vaccines; immune responses elicited by such vaccines are often of greater magnitude and of longer duration than those produced by non-replicating immunogens. One explanation for this may be that live attenuated strains establish limited infections in the host and mimic the early stages of natural infection. In addition, unlike killed preparations, live vaccines are able to induce potent cell- mediated responses which may be connected with their ability to replicate in antigen- presenting cells, such as macrophages.

There has been a long history of the use of live attenuated *Salmonella* vaccines as safe and effective vaccines for the prevention of salmonellosis in animals and humans. Indeed, the live attenuated oral typhoid vaccine, Ty21a (Vivotif), manufactured by the Swiss Serum Vaccine Institute, has proved to be a very successful vaccine for the prevention of typhoid fever and has been licensed in many countries including the US and Europe.

However, the attenuation of this strain was achieved using chemical mutagenesis techniques and the basis of attenuation of the strain is not fully understood. Because of this, the vaccine is not ideal in terms of the number of doses (currently four) and the number of live organisms that have to be given at each dose.

Modern molecular biology techniques, coupled with the increasing knowledge of *Salmonella* pathogenesis, has led to the identification of several genes that are essential for the *in vivo* growth and survival of the organisms. This has provided new gene targets for attenuation, leading to the concept that future vaccine strains can be 'rationally' attenuated by introducing defined non-reverting mutations into selected genes known to be involved in virulence. This will facilitate the development of improved vaccines, particularly in terms of the immunogenicity and therefore the number of doses that have to be given

Although many attenuated strains of *Salmonella* are now known, few have qualified as potential vaccine candidates for use in humans. This may be due in part

to the need to balance the immunogenicity of the vaccine with the possibility of the *Salmonella* microorganism becoming reactive

It is clear that the selection of appropriate targets for attenuation which will result in a suitable vaccine candidate, is not straightforward and cannot easily be predicted. Many factors may influence the suitability of the attenuated strain as an appropriate vaccine, and there is much research being carried out to identify suitable strains. For example, many attenuated strains tested as vaccine candidates lead to vaccinemia or abscesses in the patient.

It is therefore desirable to develop a vaccine having a high degree of immunogenicity with reduced possibility of the microorganism strain reverting to an reactive form and which exhibits a good safety profile with limited side effects

Summary of the Invention

The present invention is based on the finding that two specific attenuating mutations introduced into a *Salmonella* microorganism can produce a vaccine having a high degree of immunogenicity and a low risk of the microorganism reverting to a reactive form. The resulting vaccine strains exhibit a good side-effect profile.

The first mutation is contained within a region of the *Salmonella* pathogenicity island two (Spi2), the second is an auxotrophic mutation, i.e. a mutation to disrupt the expression of a gene that encodes a protein required in a biosynthetic pathway.

According to a first aspect of the invention, a *Salmonella* microorganism has an attenuating mutation which disrupts the expression of a gene located within the Spi2 pathogenicity island, and an independent auxotrophic mutation. The preferred attenuating mutation is within the apparatus gene *ssaV*, and the preferred auxotrophic mutation is within *aroC*.

The microorganism preferably further comprises one or more heterologous antigens or therapeutic proteins, for example antigens for pathogenic *E. coli*, *Shigella*, hepatitis A, B or C, Herpes Simplex Virus and Human papilloma virus. Therefore, the microorganism may act as a delivery vehicle to immunise against infections other than *Salmonella*.

The *Salmonella* microorganisms may be used to manufacture a vaccine composition which may be administered to a patient via the intravenous or oral route, in a method for the treatment of a bacterial or viral infection, e.g. for the treatment of typhoid.

The attenuated *Salmonella* microorganisms of the present invention form vaccines which surprisingly stimulate mucosal as well as systemic immunity. Further, the microorganisms do not cause spleen abscesses in an animal model, whereas mutants with single mutations do. This is a particular advantage of the double mutants as defined herein.

Description of the Invention

The microorganisms and vaccine compositions of the present invention may be prepared by known techniques.

The choice of particular *Salmonella* microorganism and the selection of the appropriate mutation, can be made by the skilled person without undue experimentation. A preferred microorganism is *Salmonella typhimurium*.

A first mutation may be introduced into a gene located within the region of the *Salmonella* pathogenicity island 2, this region being disclosed in WO-A-9617951

The *Salmonella* pathogenicity island two (Spi2) is one of two classical pathogenicity islands located on the *Salmonella* chromosome. Spi2 comprises several genes that encode a type III secretion system involved in transporting Spi2 encoded virulence-associated proteins (so-called effector proteins) outside of the *Salmonella* bacteria and potentially directly into target host cells such as macrophages. Part of Spi2 (the apparatus genes) encodes the secretion apparatus of the type III system. Spi2 is absolutely essential for the pathogenesis and virulence of *Salmonella* in the mouse, an observation now documented by several different groups around the world. *S. typhimurium* Spi2 mutants are highly attenuated in mice challenged by the oral, intravenous and intraperitoneal routes of administration.

The Spi2 gene may be either an apparatus gene or an effector gene. Preferably, the gene is an apparatus gene. The apparatus genes located within Spi2 are now well characterised; see for example Hensel *et al*, Molecular Microbiology (1997); 24(1): 155-167 Genes suitable for use in the present invention include *ssaV*, *ssaJ*, *ssaK*, *ssaL*, *ssaM*, *ssaO*, *ssaP*, *ssaQ*, *ssaR*, *ssaS*, *ssaT*, *ssaU* and *ssaH* genes.

The mutation in the Spi2 region does not necessarily have to be within a gene to disrupt the function. For example, a mutation in an upstream regulatory region may also disrupt gene expression, leading to attenuation. Mutations in an intergenic region may also be sufficient to disrupt gene function.

In a preferred embodiment of the invention, the apparatus gene is *ssaV*. In a separate preferred embodiment, the mutation lies within an intergenic region between *ssaJ* and *ssaK*

The second mutation is termed an "auxotrophic mutation" as it disrupts a gene which is essential in a biosynthetic pathway. The biosynthetic pathway is one present in *Salmonella*, but not present in mammals. Therefore, the mutants cannot depend on metabolites found in the treated patient to circumvent the effect of the mutation. Suitable genes for the auxotrophic mutation, include any *aro* gene, e.g. *aro*A, *aro*C, *aro*D and *aro*E.

In a preferred embodiment of the invention, the vaccine composition comprises a *Salmonella* microorganism having attenuating mutations in ssaV and *aro*C.

The mutations may be introduced into the microorganism using any known technique. Preferably, the mutation is a deletion mutation, where disruption of the gene is caused by the excision of nucleic acids. Alternatively, mutations may be introduced by the insertion of nucleic acids or by point mutations. Methods for introducing the mutations into the specific regions will be apparent to the skilled person.

In addition to the two mutations, the *Salmonella* microorganism may also comprise heterologous antigens. The attenuated microorganism can therefore act as a delivery vehicle for administering antigens against other bacterial or viral infections. Antigens which are suitable for use in this way will be apparent to the skilled person and include:

Pathogenic *E. coli* antigens, i.e. ETEC

Hepatitis A, B and C antigens

Lime disease antigens

vibrio cholera antigens

Helicobacter antigens

Herpes Siimplex virus antigens

Human papilloma virus antigens

This system also has the potential to deliver therapeutic proteins, e.g. cytokines, for the treatment of patients, e.g. patients infected with hepatitis. Methods for the delivery of heterologous antigens or therapeutic proteins using the vaccine compositions will be apparent to the skilled person.

Vaccines made using the microorganisms of the invention have application to the treatment of infections in human patients and in the treatment of veterinary infections.

The double mutation provides an effective means to attenuate the microorganism to provide a safe vaccine candidate.

The vaccine compositions provide effective protection even in immunocompromised patients, and importantly offer a low risk in developing spleen abscesses. Spleen abscesses have been identified using vaccines based on a single mutation, and therefore the present compositions may offer a substantial benefit to patients.

To formulate the vaccine compositions, the mutant microorganisms may be present in a composition together with any suitable pharmaceutically acceptable adjuvant, diluent or excipient. Suitable formulations will be apparent to the skilled person. The formulations may be developed for any suitable means of administration. Preferred administration is via the oral or intravenous routes and the vaccines are live attenuated *Salmonella* microorganisms. The number of microorganisms that are required to be present in the formulations can be determined and optimised by the skilled person. However, in general, a patient may be administered approximately 10^7-10^{10} CFUs, preferably approximately 10^8-10^9 CFUs in a single dosage unit.

The following Examples illustrate the invention.

Example 1

This Example describes the preparation of a mutant strain designated ZH9 which has activity as a human oral typhoid vaccine. The strain is derived from the virulent *S. typhi* strain Ty2, originally isolated from a case of typhoid. The derived strain has a defined mutation within *purA* and *aroA*.

Ty2 for the construction of ZH9

S. typni Ty2 was originally isolated from an individual with typhoid fever in 1916 and has been used for the derivation of all licensed typhoid vaccines. The strain was obtained from the PHLS national culture collection at Colindale. It was obtained as a lyophilised culture, the NCTC number being 8385.

Cloning the *S.typhi aroC* gene from *S. typhi* Ty2

S. typni Ty2 was recovered from stock and grown overnight in Luna Bertani (LB) broth. The cells were harvested and whole cell DNA was prepared. DNA fragments of *S. typni* Ty2 DNA were generated by partial cleavage with the restriction

enzyme *Sau*3A and the resulting fragments were ligated to *Bam*H1 cleaved pHC79 to generate a cosmid library of *S. typhi* Ty2 DNA using *E. coli* HU635 as recipient. To isolate the DNA encoding *aroC* from the *S. typhi* DNA, the cosmid library was used to transduce *E.coli* AB2849 which harbours a mutation in the *aroC* gene and is dependant on aromatic compounds for growth. The transduction mixture was plated onto minimal medium lacking aromatic compounds and incubated at 37°C. A number of isolated colonies were observed following overnight incubation. These bacteria had presumably arisen as a consequence of complementation of the *aroC* mutation in AB2849 by a cosmid clone harbouring the intact *aroC* gene from. Cosmid DNA from one of these strains was purified. A 5.2kb *Hind*III fragment from this cosmid was cloned into pUC18 to give plasmid pTAC2 which was able to complement the deletion of *aroC* in AB2849, demonstrating that it contains the *S.typhi aroC* gene

Generation of a defined deletion of the cloned *S. typhi* Ty2 *aroC*

A defined 600bp deletion was created within the cloned *aroC* gene using PCR. The oligonucleotide primers used in the PCR were designed using the published DNA sequence of the *S.typhi aroC* gene (Acc. M27715). The DNA 5' to the *aroC* gene was amplified from pTAC2 using primers SEQ ID NO. 3 and SEQ ID NO. 1. SEQ ID NO 3 anneals to vector DNA, SEQ ID NO. 1 anneals to the 5' region of *aroC*. The DNA 3' to the *aroC* gene was amplified using primers SEQ ID NO. 4 and SEQ ID NO 2 SEQ ID NO. 4 anneals to vector DNA, SEQ ID NO 2 anneals to the 3' region of aroC. The resulting PCR products had *Xba*I sites incorporated into the 5' ends to facilitate cloning. The fragments were cloned into the vector pUC18 The final plasmid construct designated pMIAC23 contains a defined deletion of *aroC* (position 544 to 1143) on a 4.8 kb *Hind*III fragment. The *Hind*III fragment is inserted at the *Hind*III site of pUC18. A single *Xba*I site is present at the site of the *aroC* deletion.

Introduction of the *aroC* mutation into the *S. typhi* Ty2 genome

The suicide plasmid pCVD442 (Donnenberg & Kaper, Infection and Immunity, 1991; 59: 4310-4317) was used as a vector to introduce the *aroC* deletion into the genome of *S. typhi* Ty2. The 4.8kb *Hind*III fragment containing the *aroC* deletion was isolated from pMIAC23 and the ends made blunt by using the Stratagene DNA polishing kit. Plasmid pCVD442 was linearized by digestion with *Sma*I, treated with alkaline phosphatase and ligated to the blunt-ended fragments. The required construct was isolated and denoted pYCVC21

pYCVC21 was introduced into *S typhi* Ty2 by using a standard electroporation protocol. The plasmid was able to integrate into the Ty2 genome following recombination between the homologous regions on the plasmid and the genome to give ampicillin resistant transformants. These transformants contained a copy of both the original wild type *aroC* and the deleted *aroC* gene Growing these strains in the absence of ampicillin allowed for a second recombination event to occur which resulted in loss of the pCVD442 DNA sequences and one copy of the *aroC* gene, either the wild-type copy or the deleted copy. *S. typhi* Ty2 bacteria which had undergone this second recombination event were identified as ampicillin sensitive derivatives which were able to grow in the presence of 5% sucrose (pCVD442 carries the *sacB* gene which when expressed results in a sucrose sensitive phenotype). Strains that had retained only the deleted *aroC* gene were initially identified as strains that were unable to grow on minimal media plates in the absence of a supplement of aromatic compounds The *aroC* genotype was confirmed by using PCR analysis Primers having SEQ ID NO 5 and SEQ ID NO. 6 gave a product of 994bp for the wild type *aroC* and 400bp for the deleted *aroC* gene. Sequence analysis of the resulting PCR products confirmed the presence of the required deletion in 5 individual isolates designated DTY6, DTY7, DTY8, DTY9 and DTY10. These strains were stored in Microbank vials at -70°C for long term storage. Strain DTY8 was chosen for further manipulation.

Introduction of an *ssaV* mutation into the *S. typhi aroC* mutant DTY8

A 7.5 kb PstI fragment containing the *ssaV* region of *S. typhi* was amplified from a total DNA preparation by using PCR and cloned into the vector pCR2 1 (Invitrogen). The PCR oligonucleotide primers employed, having SEQ ID NO. 7 and SEQ ID NO. 8, were designed to the *S. typhimurium* SPI2 sequence. The resulting plasmid construct was designated pTYSV21.

A plasmid construct possessing a deletion of the *ssaV* gene was derived from pTYSV21 by using reverse orientation PCR. Primers annealing to the 5' (SEQ ID NO. 9) and 3' (SEQ ID NO. 10) regions of the *ssaV* open reading frame were designed to the *S. typhimurium* Spi2 sequence. An *Avr*II restriction site was incorporated into the 5' region of each primer, an *Xba*I site was incorporated into SEQ ID NO. 10. The *Xba*I site serves as a tag for the *ssa*V mutation so it can be detected easily by restriction analysis. The resulting PCR product was subjected to digestion with *Avr*II and the backbone plasmid molecules purified following agarose gel electrophoresis Re-

circularisation of the resulting fragments at the *Avr*II sticky-ends gave the required deletion construct pYDSV1. pYDSV1 contains a 5.5kb PstI fragment with a defined 1894bp deletion within the *ssaV* open reading frame.

The suicide plasmid pCVD442 was used as a vector to introduce the *ssaV* deletion into the genome of the *S. typhi* Ty2 *aroC* mutant DTY8. The 5.5kb *Pst*I fragment containing the *ssaV* deletion was isolated from pYDSV1 and the ends made blunt by treatment with Klenow DNA polymerase. Plasmid pCVD442 was linearized by digestion with *Sma*I, treated with alkaline phosphatase and ligated to the blunt-ended fragments. The required construct was isolated and denoted pYDSV214.

pYDSV214 was introduced into *S. typhi* DTY8 by using electroporation. Ampicillin-resistant transformants were selected and then grown in the absence of ampicillin to allow for loss of the pCVD442 DNA sequences and one copy of the *ssaV* gene, either the wild-type copy or the deleted copy. Strains that had undergone this second recombination event were identified as ampicillin-sensitive, sucrose-resistant colonies. Strains that had retained only the deleted *ssaV* gene were identified by using PCR analysis. Primers having SEQ ID NO. 11 and SEQ ID NO 12 gave a product of 2485bp for the wild type *ssaV* and 591bp for the deleted *ssaV* gene. Sequence analysis of the resulting PCR products confirmed the presence of the required deletion in 5 individual isolates, ZH2, ZH4, ZH6, ZH7 and ZH9. STrain ZH9 was chosen for manufacture of a CGMP master cell bank.

Example 2

This Example describes the preparation of a *S. typhimurium* mutant strain designated WT05 which has vaccine activity against human gastroenteritis. The strain is derived from the known human virulent *S. typhimurium* strain TML.

TML for the construction of WT05

TML was originally isolated from a patient suffering from gastroenteritis and was identified in the laboratories of Dr John Stevens at Birmingham University. It was lyophilised at Wellcome Research Laboratories and assigned a culture number, BRD 519. The culture was obtained from Birmingham University.

Generation of a defined deletion of the cloned *S. typhimurium ssaV* gene

A plasmid (plasmid 7-2, Shea *et al*; PNAS, 1996; 93: 2593-2597) was generated by cloning a 7.5kb *Pst*I fragment isolated from *S. typhimurium* LT2 into the *Pst*I site of pUC18. *ssaV* is positioned centrally on this fragment. A plasmid construct containing a defined deletion of the *ssaV* ORF was derived from plasmid 7-2 by using

reverse orientation PCR. Primers annealing to the 5' (SEQ ID NO. 13) and 3' (SEQ ID NO. 14) regions of the *ssaV* open reading frame were designed to the *S.typnimurium* Spi2 sequence. An *Avr*II restriction site was incorporated into the 5' region of each primer and an *Xba*I site was incorporated into SEQ ID NO. 14. The *Xba*I site serves as a tag for the *ssaV* mutation so it can be detected easily by restriction analysis. The resulting PCR product was subjected to digestion with *Avr*II and the backbone plasmid molecules purified following agarose gel electrophoresis. Re-circularisation of the resulting fragments at the *Avr*II sticky-ends gave the required deletion construct designated pMDSV1. pMDSV1 contains a 5.5kb *Pst*I fragment with a defined 1894bp deletion within the *ssaV* open reading frame. An *Avr*II and a *Xba*I restriction site are at the site of the deletion.

The suicide plasmid pCVD442 was used as a vector to introduce the *ssaV* deletion into the genome of *S. typnimurium* TML. The 5.5kb *Pst*I fragment containing the *ssaV* deletion was isolated from pMDSV1 and the ends made blunt by treatment with Klenow DNA polymerase. Plasmid pCVD442 was linearized by digestion with *Sma*I, treated with alkaline phosphatase and ligated to the blunt-ended fragments. The required construct was isolated and denoted pMDSV22.

pMDSV22 was introduced into *S. typnimurium* TML using conjugation. To this end the construct was transformed into the *E. coli* strain S17-1 λpir. The conjugation was performed according to standard procedures. Plasmid pMDSV22 was able to integrate into the TML genome following recombination between the homologous regions on the plasmid and the genome to give ampicillin resistant transconjugants. A transconjugate designated mdsv-WT2 was chosen for further manipulations. This transconjugant contains a copy of both the original wild-type *ssaV* and the deleted *ssaV* gene. It was grown in the absence of ampicillin to allow for a second recombination event to occur which would result in the loss of the pCVD442 DNA sequences and one copy of the *ssaV* gene, either the wild-type copy or the deleted copy. Isolates which had undergone this second recombination event were identified as ampicillin-sensitive derivatives which were able to grow in the presence of 5% sucrose (pCVD442 carries the *sacB* gene which when expressed results in a sucrose-sensitive phenotype). Strains that had retained only the deleted *ssaV* gene were identified by using PCR analysis. Primers having SEQ ID NO. 15 and SEQ ID NO 16 gave a product of 2485bp for the wild type *ssaV* and 591bp for the deleted *ssaV* gene. Sequence analysis of the resulting PCR products confirmed the presence of the

required deletion in 4 individual isolates, ZH20, ZH23, ZH25 and ZH26. These strains were stored in LB plus 15% glycerol at –80°C for long-term storage Strain ZH26 was chosen for further manipulation.

Cloning the *S.typhimurium aroC* gene from *S. typhimurium* TML

Genomic DNA was isolated from *S. typhimurium* TML and cleaved with *Hind*III *Hind*III fragments in the size range 5 to 6kb were purified and ligated to *Hind*III-cleaved pBluescript. The ligation mixture was used to transform an *E. coli aroC* mutant, AB2849, and clones containing the *S. typhimurium aroC* gene were selected by virtue of their ability to complement this strain. Analysis of one clone, pDAC1, demonstrated that it contained a 5.2kb *Hind*III fragment

A defined 600bp deletion was created within the cloned *aroC* gene by using PCR. The oligonucleotide primers were designed using the published DNA sequence of the *S. typhi aroC* gene (Acc M27715) The DNA 5' to the *aroC* gene was amplified from pDAC1 using primers having SEQ ID NO. 19 and SEQ ID NO. 17. SEQ ID NO 19 anneals to vector DNA, SEQ ID NO. 17 anneals to the 5' region of *aroC*. The DNA 3' to the *aroC* gene was amplified using primers having SEQ ID NO. 20 and SEQ ID NO. 18. SEQ ID NO. 20 anneals to vector DNA, SEQ ID NO. 18 anneals to the 3' region of *aroC*. The resulting PCR products had *Xba*I sites incorporated into the 5' ends to facilitate cloning. The fragments were cloned into the vector pUC18. The final plasmid construct pMIAC8 contains a defined deletion of *aroC* (Acc. M27715 position 544 to 1143) on a 4.8 kb *Hind*III fragment. The *Hind*III fragment is inserted at the *Hind*III site of pUC18. A single *Xba*I site is present at the site of the deletion.

Introduction of the *aroC* mutation into the *S. typhimurium ssaV* mutant ZH26

The suicide plasmid pCVD442 was used as the vector to introduce the *aroC* deletion into the genome of *S. typhimurium* TML. The 4.8kb *Hind*III fragment containing the *aroC* deletion was isolated from pMIAC8 and the ends made blunt by using the Stratagene DNA polishing kit (Part No. 200409). Plasmid pCVD442 was linearized by digestion with *Sma*I, treated with alkaline phosphatase and ligated to the blunt-ended fragments. The required construct was isolated and denoted pMCVC16 pMCVC16 was introduced into *S. typhimurium* ZH26 by using electroporation. Ampicillin-resistant transformants were selected and allowed to grow in the absence of ampicillin to allow for loss of the pCVD442 DNA sequences and one copy of the *aroC* gene, either the wild-type copy or the deleted copy. Strains that had undergone this second recombination event were identified as ampicillin-sensitive derivatives that

were able to grow in the presence of 5% sucrose. Strains that had retained only the deleted *aroC* gene were initially identified as strains that were unable to grow on minimal media plates in the absence of a supplement of aromatic compounds. The *aroC* genotype was confirmed by using PCR analysis. Primers having SEQ ID NO. 21 and SEQ ID NO. 22 give a product of 994bp for the wild type *aroC* and 400bp for the deleted *aroC* gene. Sequence analysis of the resulting PCR products confirmed the presence of the required deletion in 4 individual isolates designated WT05, WT09, WT10 and WT12. Strain WT05 was chosen for manufacture of a CGMP master cell bank.

Example 3

The following construct was prepared to test the double mutant vaccines in an animal model. *S. typhimurium* SL1344, a strain that infects mice, was used, with single and double mutations present.

An *ssaV::aph* (non-polar) mutation from *S. typhimurium* 12023s was P22 transduced to SL1344 to give the single Spi2 mutant.

The *aroC* deletion/pCVD422 suicide vector pMCVC16 was electroporated into the *S. typhimurium* strain LB5010 and merodiploids were obtained. The *aroC* deletion merodiploid was then P22 transduced from the LB5010 merodiploid to SL1344. The SL1344 merodiploid was then resolved using sucrose selection to give the single *aroC* mutant.

The double mutant was generated by P22 transduction of the *aroC* deletion merodiploid from LB5010 into the SL1344 *ssaV::aph*. Plasmid sequences were resolved from the merodiploid leaving strain 3, the *aroC* deletion mutation in the SL1344 *ssaV::aph* background.

Pre-clinical pharmacodynamic studies on defined *aroC/ssaV Salmonella* mutants

Salmonella mutants (strain SL1344) harbouring defined mutations in either *aroC*, *ssaV* or a combination of both mutations have been evaluated extensively in BALB/C mice to assess attenuation, persistence of the organisms and ability to immunise against challenge with the wild type strain.

Example 4

Animals immunised by the intravenous route

Protection studies

Groups of ten BALB/C mice were immunised i.v. with 10^5 and 10^6 organisms of SL1344 *aroC*, SL1344 *ssaV*, and SL1344 *aroC*: *ssaV* grown overnight in LB broth

and resuspended in saline for administration. Mice were challenged 6 weeks later with 10^5 wild type organisms given intravenously. Ten organisms of this wild type strain given intravenously are sufficient to kill mice.

All the mice given the single *aro*C or *ssa*V mutants were solidly protected after challenge with either dose and remained well throughout the experiment, exhibiting no sign of disease. For the double mutant 90% of the animals were solidly protected that received the immunisation with 10^8 organisms. One of the animals died 8 days after the challenge. For the animals that were immunised with the lower dose, only 1 of the mice survived the challenge.

This experiment demonstrates that immunisation with *Salmonella ssa*V mutants, either alone, or in combination with an *aro*C mutation will immunise mice against challenge with the wild type *Salmonella* strain.

Persistence of Strains

Groups of mice were given 10^5 organisms of the three *Salmonella* mutants described above. Four mice were sacrificed at different time points up to day 14 and enumeration of organisms in livers and spleens were performed. Counts of all three mutants were comparable up until day 10 when the counts were approximately 5×10^5 organisms in each organ. At day 14 a difference was demonstrated between the single mutants and the double mutants, there being a log less in the numbers of double mutant organisms in both liver and spleens.

The other important difference between the single mutant and the *aro*C/*ssa*V double mutant is that there were no liver abscesses present at any time during the experiment for the double mutants. However, the mice infected with the single mutants did have liver abscesses present at day 10 and 14. This is an important finding and strongly supports the use of this combination of mutations for evaluation the preparation of vaccines.

Immunogenicity

Mice immunised as above were bled and the antibody titres were determined against whole cell *Salmonella* using an ELISA. All three strains were demonstrated to be highly immunogenic, eliciting high titres of circulating IgG against *Salmonella*.

Example 5

Animals immunised by the oral route

Persistence of strains

Groups of mice immunised orally with 5 x 10^8 organisms of each of the three *Salmonella* mutants were sacrificed at periodic intervals and the numbers of organisms enumerated in livers and spleens. For the single *aro* mutant and the single *ssaV* mutant counts in livers and spleens were 10^5 and 10^2 respectively up until about day 21. Thereafter the numbers reduced. For the mice that received the *aroC. ssaV* double mutants, organisms were virtually undetectable in the livers and spleens after oral immunisation.

Oral immunisation and intravenous challenge of A-J mice vaccinated with *Salmonella typhimurium* TML *aroC/ssaV* (WT05).

The purpose of this experiment was to ascertain the protective efficacy of 5 x 10^8 *aroC/ssaV S. typnimurium* TML mutants in an oral ity^r murine vaccination and intravenous challenge model. This model more closely resembles the human response to *Salmonella* in that these animals are less susceptible than an ity^s backgrounc.

5 x 10^8 *S. typnimurium* TML *aroC/ssaV* in a volume of 0.2 ml PBS was inoculated orally by gavage tube into 10 6-8 week old A-J mice and left 8 weeks. Two mice were given PBS only at this time and served as control animals. After 8 weeks had elapsed the two immunised groups were challenged intravenously with 10^7 wild type *S. typhimurium* TML. Mice were observed for 30 days post challenge

All animals were solidly protected against wild type challenge (100% survival, 10/10 animals alive). Mice given PBS alone and then challenged with wild type *S typhimurium* TML died on day 6 post challenge

In an ity^r background the double *S. typhimurium* TML aroC/ssaV seems to protect mice given an oral dose of 5 x 10^8. This may be important for the human situation as ity^r mice are a better model of human salmonellosis, in terms of susceptibility to infection.

Studies were also carried out to evaluate the persistence of the double mutants in the livers and spleens of the mice. It was found that the double mutants persist at low levels to around day 21. By day 28, the mutant strain has been cleared

Example 6

Human clinical trial

18 healthy volunteers were recruited to an open label, non-placebo controlled study. Following appropriate screening, each of 3 volunteers received a single oral dose of either 10^7, 10^8 or 10^9 CFUs of *S.typhi* ZH9 or *S. typhimurium* WT05 The microorganisms prepared as above were resuspended to the appropriate dosing

concentrations in a final volume of 100ml of 2% (w/v) sodium bicarbonate solution to neutralize gastric acid. This liquid suspension was administered orally to the volunteers. The volunteers were then isolated for 72 hours, and then followed up post immunisation for safety and immunogenicity.

Volunteers were assessed for reactogenicity and other adverse events associated with vaccination by observation, physical examination and by the completion of diary cards. In addition, blood, stool and urine cultures were collected to assay for vaccinaemia, shedding and persistence of the vaccine strains. Additional safety data was obtained by measuring levels of C-reactive protein (CRP) and liver function enzymes (ALT) in blood, total white blood cell (WBC) counts and erythrocyte sedimentation rates (ESR) using standard procedures. These parameters were measured on blood taken daily until day 7 and then at weekly intervals until day 28.

Analysis of mucosal and systemic immune responses

Blood and saliva samples were collected prior to immunization and then on days, 7, 14, 21 and 28 after immunization, Saliva and serum were frozen at -70°C until analysis by ELISA. Peripheral blood mononuclear cells were collected and assayed for the presence of antibody-secreting cells (ASCs) using the ELISPOT technique

Both *S. typhi* ZH9 and *S. typhimurium* WT05 were well tolerated in all of the volunteers. No serious adverse events were noted in any of the volunteers at each of the 3 dose levels and blood and urine cultures remained negative in all vaccinees at all time-points examined. Thus, immunisation with both *S. typhi* ZH9 and *S. typhimurium* WT05 do not result in vaccinaemias. None of the volunteers given either of the strains developed diarrhoea or persistent high-grade fever, further indicating the safety of the vaccine strains Persistent excretion nor vaccinaemia beyond day 7 was not observed in either of the 3 dose groups of *S. typhi* ZH9 or in the low dose (10^7) of *S. typhimurium* WT05.

Mucosal and systemic immune responses elicited by *S. typhi* ZH9

Oral immunization with a single low dose (1×10^7 CFUs) of *S. typhi* ZH9 resulted in the priming of *S. typhi*–specific IgA-secreting ASCs in 2 of 3 volunteers detected 7 days after immunization. Subsequent testing on days 14 and 21 showed that IgA ASCs were still detectable but at much lower levels and had disappeared by day 28 In almost all responder vaccinees, numbers of ASCs were highest on day 7. Surprisingly, ingestion of a higher dose (10^8 CFUs) of *S. typhi* ZH9 resulted in a low IgA ASC response in only one of three vaccinees. Ingestion of the highest dose (1×10^9 CFUs) primed IgA ASCs in 2 of 3 volunteers

Salmonella-specific serum antibody response

Oral immunization with a single low dose (1×10^7 CFUs) of *S. typhi* ZH9 failed to elicit *S. typhi* LPS-specific serum IgG (despite generating IgA-ASCs in 2/3 vaccinees) when examined on days 7, 14, 21 and 28. Similarly only 1/3 produced very low levels of flagella-specific IgG. However, ingestion of 10^8 CFUs resulted in the production of high levels of both LPS and flagella-specific IgG in all 3 volunteers. Increased levels of *S. typhi* LPS specific and flagella-specific were detected as early as 7 days after vaccination, rising on day 14 and remaining high on day 28. The highest dose of 10^9 CFUs also stimulated LPS- and flagella-specific IgG in 2 of 3 vaccinees, detectable on days 7 and 14 respectively.

Conclusions

This study demonstrated the utility of the *ssaV* mutation, as a component of any new oral typhoid vaccine strain. An *S.typhi* strain harbouring *aro* mutations alone would have caused vaccinaemias at the doses given. The ssaV mutation therefore provides an additional level of safety to the *aro* mutation alone by abolishing the vaccinaemias using this early formulation.

As well as proving to be well-tolerated, ZH9 was also demonstrated to be immunogenic at all three dose levels given. With regard to stimulating serum antibody, the intermediate (10^8 CFUs) and highest (10^9 CFUs) doses proved to be highly immunogenic, with 3/3 vaccines given 10^8 CFUs and 2/3 given 10^9 CFUs eliciting high titres of both *S. typhi* LPS and flagella specific-serum IgG. These responses are very encouraging since it is generally difficult to elicit serum antibody by oral vaccination.

As well as generating *S. typhi*-specific serum antibody responses, ZH9 also primed IgA ASCs, indicative of immune stimulation at the intestinal mucosa. A total of 5/9 volunteers elicited an *S.typhi* LPS-specific IgA-secreting cell (ASC) response which did not appear to be dose-dependent.

WT05 was also well tolerated and no vaccinaemias were detected. Interestingly, no diarrhoeas or symptoms of gastroenteritis were detected in any of volunteers. The previous data obtained using the mutant TML strain with single aro or SPI 2 mutations in *S typhimurium* given to mice suggested that a double *aroC/ssaV* mutant might cause some local intestinal effects e.g. diarrhoea, cramps in humans. The absence of these events further supports the utility of the combination of aro and SPI2 mutations.

Example 7

Heterologous antigen carriers

To demonstrate the utility of the *ssaV:aroC* double mutant strains to express and deliver foreign antigens, WT05 was transformed with a plasmid (pBRDO26) expressing the gene for the *E. coli* heat-labile enterotoxin B subunit (LT-B).

BALB/C mice (n=10/group) were immunised orally on days 0 and 28 with 10^9CFUs (200ml in PBS) WT05 expressing pBRD026, or with the WT05 vector strain (control). For comparison (and as a positive control) a group of mice (n=5) were immunised orally on days 0 and 28 with 10 µg purified LT (Sigma). Negative control mice (n=5) were immunise orally on days 0 and 28 with 200 µl PBS. Mice were bled from the tail vein on days 21, 28, 35 and by cardiac puncture on day 42 and sera and intestinal lavage (day 42 only) collected and stored at -20°C.

All but one of the mice immunised with WT05/LT-B elicited LT-specific IgG (titres of 3,000-50,000) on day 28 after a single oral dose. None of the control mice immunisec orally with WT05 or PBS elicited LT-specific IgG. Oral immunisation with a single dose of purified LT elicited higher titres of LT-specific antibody (titres of 6,000->50,000) When the isotype of the LT-B-specific serum IgG was examined, it was found that the WT05 strain expressing pBRD026 elicited almost exclusively LT-specific IgG2a, indicating a bias towards a TH1-type immune response. In contrast, mice immunized with purified LT (Sigma) elicited almost exclusively LT-specific IgG1, indicating a TH2-type response. Therefore, expressing the LT-B within the *aroC/ssaV* strain facilitates profound immune modulation. The TH1-biased responses generated by the *Salmonella* aroC/ssaV strain will be important when antigens from pathogenic organisms for which TH1-type responses are protective, are expressed.